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**RAW SEQUENCE LISTING
ERROR REPORT**

BIO TECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/595,526

Source: 1645

Date Processed by STIC: 9-6-00

RECEIVED

SEP 28 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/395,526

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length
Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
Indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 Skipped Sequences (OLD RULES)
Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES)
Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <213>Organism (NEW RULES)
Sequence(s) are missing this mandatory field or its response.

12 Use of <220>Feature (NEW RULES)
Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

Re-run

1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000
TIME: 11:05:03

Input Set : A:\CVT 158.txt
Output Set: N:\CRF3\09062000\1595526.raw

5 <110> APPLICANT: Lawn, Richard M.
7 Wade, David
9 Garvin, Michael
11 Oram, John F.
15 <120> TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol
17 Efflux and Raising HDL using ATP Binding Cassette
19 Transporter Protein ABC1
23 <130> FILE REFERENCE: 99,395-A
C--> 27 <140> CURRENT APPLICATION NUMBER: US/09/595,526
C--> 29 <141> CURRENT FILING DATE: 2000-06-16
33 <150> PRIOR APPLICATION NUMBER: US 60/140,264
35 <151> PRIOR FILING DATE: 1999-06-18
39 <150> PRIOR APPLICATION NUMBER: US 60/153,872
41 <151> PRIOR FILING DATE: 1999-08-14
45 <150> PRIOR APPLICATION NUMBER: US 60/166,573
47 <151> PRIOR FILING DATE: 1999-11-19
51 <160> NUMBER OF SEQ ID NOS: 57
55 <170> SOFTWARE: PatentIn Ver. 2.0
59 <210> SEQ ID NO: 1
61 <211> LENGTH: 10442
63 <212> TYPE: DNA
65 <213> ORGANISM: Homo sapiens
69 <400> SEQUENCE: 1

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73 ggagctccgc gaccaacag agccggctt caggcggcgtt tgctccctgt ttttccccg 120
75 gttctgtttt ctcccccttc ccggaaaggct tgcataagggg taggaaaaag agacgcacaaac 180
77 acaaaagtgg aaaaacagtta atgaccagcc acggggcgctc ctgctgttag ctctggccgc 240
79 tgcctccag ggctcccgg ccacacgctg ggctgtctgg ctgagggaaat atggcttgg 300
81 ggcctcagct gaggtgtcg ctgtggaaat actctcaactt cagaagaaga caaacatgtc 360
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97 tcccaaagtcc tactgtggac aagatgtga ggctgtatgtt cattttccac aaggatatttt 840
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101 ttcaacttgg tgaccaagaa gtttctggc tttgtggcctt accaaaggag aaactggctg 960
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107 gtcttggac tctggcccg gacgtgttca gcatgagaag ctggagtgtac atgcgacagg 1140
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111 tgcctctat tgcgtcgccg catcccgagg gagggggggctt gaaagatcaag tctctcaact 1260
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115 aaacccctta tgaccaactt acaactccctt actgtcaatgtt tttgtatgaat aatttggagt 1380
117 ctatgttccatc ttcccgattt atctggaaat ctgtcaagcc gctgtcggtt gggaaatcc 1440

Does Not Comply
Corrected Diskette Needed

Sec P. 4, 5

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000
TIME: 11:05:03

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Output Set: N:\CRF3\09062000\I595526.raw

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123 ggacccatgg gagaacacgc caagaaatgg actcttgtccg gatgtgttgc gacagcagg 1620
125 acaatgacca cttttggaa cagcagtggg actgttgcgg taggttgcgg aagacatcg 1680
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129 ggagagaacg ttcaacagc actaaccagg caatccggac catatctgc ttcatggat 1800
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133 tggagctgtt ggttggagg aagtcttggg ctggatgtt gtttactggg attactccg 1920
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139 aggacatcg gttttttttt gggggcttcg cctacttgcg gatgtgttgc gaggcagg 2100
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183 gcaagcttccaa aacccatccatcc tttttttttt tttttttttt tttttttttt 3420
185 cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 3480
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000
TIME: 11:05:03

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Output Set: N:\CRF3\09062000\I595526.raw

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000
TIME: 11:05:03

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Output Set: N:\CRF3\09062000\I595526.raw

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 387 attttttttca ttttttttttcaataacttgc tttttttttt 9540
 389 caatcaagca aatatttttttcaataacttgc tttttttttt 9600
 391 ctcaaaatc ttttttttttcaataacttgc tttttttttt 9660
 393 ttaacactg ttttttttttcaataacttgc tttttttttt 9720
 395 ccagcacat ttttttttttcaataacttgc tttttttttt 9780
 397 actgttttttcaataacttgc tttttttttt 9840
 W--> 399 atcatttgc ttttttttttcaataacttgc tttttttttt 9900
 401 attttttttttcaataacttgc tttttttttt 9960
 W--> 403 ggacccttgg ttttttttttcaataacttgc tttttttttt 10020
 W--> 405 ttttttttttcaataacttgc tttttttttt 10080
 407 ctttttttttcaataacttgc tttttttttt 10140
 409 caagcacat ttttttttttcaataacttgc tttttttttt 10200
 411 aaaacttagac aaaatgttgc tttttttttt 10260

<220> blank line
 <221> name/key
 <222> location
 <223> other info.

Missing mandatory
 <220> to <223> features
 to explain "n's" in
 sequence. See
 #10 on Error
 Summary Sheet.
 This error has
 been indicated
 elsewhere in the
 sequence listing. Please
 check and correct.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000
TIME: 11:05:03

Input Set: A:\CVT 158.txt
Output Set: N:\CRF3\09062000\I595526.raw

```

413 aaagaaaaaaaaa-aattttgtat-gtcaataact ttatataaag tattaaaatg catatttcta 10320
415 tggtaataa taatggatca caaaataaaag ctgtgacagt tctgttaaaa aaaaaaaaaa 10380
417 aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 10440
419 aa 10442
422 <210> SEQ ID NO: 2
424 <211> LENGTH: 2261
426 <212> TYPE: PRT
428 <213> ORGANISM: Homo sapiens
432 <400> SEQUENCE: 2
434 Met Ala Cys Trp Pro Gln Leu Arg Leu Leu Trp Lys Asn Leu Thr 10 15
436 1 5
440 Phe Arg Arg Arg Gln Thr Cys Gln Leu Leu Leu Glu Val Ala Trp Pro 20 25 30
442 20 25
446 Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro 35 40 45
448 35 40
452 Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala 50 55 60
454 50 55
458 Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro 65 70 75 80
460 65 70
464 Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn 85 90 95
466 85
470 Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu 100 105 110
472 100 105
476 Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val 115 120 125
478 115 120
482 Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Asn Leu Lys Leu 130 135 140
484 130 135
488 Gln Asp Phe Leu Val Asp Asn Glu Thr Phe Ser Gly Phe Leu Tyr His 145 150 155 160
490 145 150
494 Asn Leu Ser Leu Pro Lys Ser Thr Val Asp Lys Met Leu Arg Ala Asp 165 170 175
496 165
500 Val Ile Leu His Lys Val Phe Leu Gln Gly Tyr Gln Leu His Leu Thr 180 185 190
502 180 185
506 Ser Leu Cys Asn Gly Ser Lys Ser Glu Glu Met Ile Gln Leu Gly Asp 195 200 205
508 195 200
512 Gln Glu Val Ser Glu Leu Cys Gly Leu Pro Lys Glu Lys Leu Ala Ala 210 215 220
514 210
518 Ala Glu Arg Val Leu Arg Ser Asn Met Asp Ile Leu Lys Pro Ile Leu 225 230 235 240
520 225
524 Arg Thr Leu Asn Ser Thr Ser Pro Phe Pro Ser Lys Glu Leu Ala Glu 245 250 255
526 245
530 Ala Thr Lys Thr Leu Leu His Ser Leu Gly Thr Leu Ala Gln Glu Leu 260 265 270
532 260
536 Phe Ser Met Arg Ser Trp Ser Asp Met Arg Gln Glu Val Met Phe Leu 275 280 285
538 275
542 Thr Asn Val Asn Ser Ser Ser Ser Thr Gln Ile Tyr Gln Ala Val 290 295 300
544 290
548 Ser Arg Ile Val Cys Gly His Pro Glu Gly Gly Leu Lys Ile Lys 305 310 315 320
550 305

```

F.Y. 1.
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/595,526

DATE: 09/06/2000
TIME: 11:05:04

Input Set : A:\CVT 158.txt
Output Set: N:\CRF3\09062000\1595526.raw

L:27 M:270 C: Current Application Number differs, Replaced Application Number
L:29 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:399 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:399 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:399 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:399 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:399 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:403 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:403 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:403 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:403 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:405 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:405 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:405 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:405 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:1368 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:1368 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:1368 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:1368 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:1368 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:1370 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:1370 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:1370 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:1370 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:1372 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:1372 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:1372 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:1372 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:1374 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:1374 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:1374 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:1374 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:1580 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:1580 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:1580 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:1580 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:1580 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:1584 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:1584 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:1584 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:1584 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:1586 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:1586 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:1586 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:1586 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6

VERIFICATION SUMMARY DATE: 09/06/2000
PATENT APPLICATION: US/09/595,526 TIME: 11:05:04

Input Set.: A:\CVT.158.txt
Output Set: N:\CRF3\09062000\I595526.raw

L:1945 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:1945 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:1945 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:1945 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:1945 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:1949 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:1949 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:1949 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:1949 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
M:340 Repeated in SeqNo=7
L:3173 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:3173 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:3173 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
M:340 Repeated in SeqNo=9